

RAW SEQUENCE LISTING ERROR REPORT

BIO

TECHNOLOGY

SYSTEMS

BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/680,121

Source: OIPE

Date Processed by STIC: 10-18-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/680,121</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	<u>Use of n's and/or Xaa's have been detected in the Sequence Listing.</u> <u>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.</u> <u>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</u>	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/680,121

DATE: 10/18/2000
TIME: 17:20:29

Input Set : A:\Mueth31.app
Output Set: N:\CRF3\10182000\I680121.raw

```

3 <110> APPLICANT: French, Cynthia K.
4 Schneider, Patrick A.
5 Yamamoto, Karen K.
7 <120> TITLE OF INVENTION: Prostate Cancer-Specific Marker
9 <130> FILE REFERENCE: 107-206-C
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/680,121
12 <141> CURRENT FILING DATE: 2000-10-04
14 <150> PRIOR APPLICATION NUMBER: 60/041,246
15 <151> PRIOR FILING DATE: 1997-03-07
17 <150> PRIOR APPLICATION NUMBER: 60/047,811
18 <151> PRIOR FILING DATE: 1997-05-15
20 <150> PRIOR APPLICATION NUMBER: 09/036,315
21 <151> PRIOR FILING DATE: 1998-03-06
23 <150> PRIOR APPLICATION NUMBER: 09/535,597
24 <151> PRIOR FILING DATE: 2000-03-27
26 <160> NUMBER OF SEQ ID NOS: 27
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 3891
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (151)..(1425)
39 <220> FEATURE:
40 <223> OTHER INFORMATION: product = Repro-PC-1.0
42 <400> SEQUENCE: 1
43 ctctttgcct ctcctcgtt ccaggagctg gtgcctggg ctctgcgttg ttgtttcag 60
45 cggtccggaaa gcccggcggtt gagatccagg caagtgaatc cagccaggca gttttccctt 120
47 cagcacccgt gacagaacac gcagaaaaaa atg gct ccg atc acc acc agc cgg 174
48 Met Ala Pro Ile Thr Thr Ser Arg
49 1 5
51 gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
52 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
53 10 15 20
55 ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 270
56 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
57 25 30 35 40
59 aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
60 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
61 45 50 55
63 ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
64 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys Lys
65 60 65 70
67 ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 414
68 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
69 75 80 85

```

Does Not Comply
Corrected Diskette Needed

see p 6

RAW SEQUENCE LISTING DATE: 10/18/2000
 PATENT APPLICATION: US/09/680,121 TIME: 17:20:29

Input Set : A:\Mueth31.app
 Output Set: N:\CRF3\10182000\I680121.raw

71	aag aat tca ttg cat ctg gat ctt gaa aag aga gat ctc aat ggc aat	462
72	Lys Asn Ser Leu His Leu Asp Leu Glu Lys Arg Asp Leu Asn Gly Asn	
73	90 95 100	
75	ttt ccc aaa acc aac ctc aaa cct ggc agt cct tct gat ctg gag aat	510
76	Phe Pro Lys Thr Asn Leu Lys Pro Gly Ser Pro Ser Asp Leu Glu Asn	
77	105 110 115 120	
79	gca acc ccg aag ctc ttt tta gaa ggg gaa aaa gag tca gtt tcc cct	558
80	Ala Thr Pro Lys Leu Phe Leu Glu Gly Glu Lys Glu Ser Val Ser Pro	
81	125 130 135	
83	gag agt tta aag tcc agc act tcc ctt act tca gaa gag aaa caa gag	606
84	Glu Ser Leu Lys Ser Ser Thr Ser Leu Thr Ser Glu Glu Lys Gln Glu	
85	140 145 150	
87	aag ctg gga act ctc ttc ttc tcc tta gaa tac aac ttc gag aga aaa	654
88	Lys Leu Gly Thr Leu Phe Phe Ser Leu Glu Tyr Asn Phe Glu Arg Lys	
89	155 160 165	
91	gca ttt gtg gtc aat atc aag gaa gcc cgt ggc ttg cca gcc atg gat	702
92	Ala Phe Val Val Asn Ile Lys Glu Ala Arg Gly Leu Pro Ala Met Asp	
93	170 175 180	
95	gag cag tcg atg acc tct gac cca tat atc aaa atg acg atc ctc cca	750
96	Glu Gln Ser Met Thr Ser Asp Pro Tyr Ile Lys Met Thr Ile Leu Pro	
97	185 190 195 200	
99	gag aag aag cat aaa gtg aaa act aga gtg ctg aga aaa acc ttg gat	798
100	Glu Lys Lys His Lys Val Lys Thr Arg Val Leu Arg Lys Thr Leu Asp	
101	205 210 215	
103	cca gct ttt gat gag acc ttt aca ttc tat ggg ata ccc tac acc caa	846
104	Pro Ala Phe Asp Glu Thr Phe Thr Phe Tyr Gly Ile Pro Tyr Thr Gln	
105	220 225 230	
107	atc caa gaa ttg gcc ttg cac ttc aca att ttg agt ttt gac agg ttt	894
108	Ile Gln Glu Leu Ala Leu His Phe Thr Ile Leu Ser Phe Asp Arg Phe	
109	235 240 245	
111	tca aga gat gat atc att ggg gaa gtt cta att cct ctc tcg gga att	942
112	Ser Arg Asp Asp Ile Ile Gly Glu Val Leu Ile Pro Leu Ser Gly Ile	
113	250 255 260	
115	gaa tta tct gaa gga aaa atg tta atg aat aga gag atc atc aag aga	990
116	Glu Leu Ser Glu Gly Lys Met Leu Met Asn Arg Glu Ile Ile Lys Arg	
117	265 270 275 280	
119	aat gtt agg aag tct tca gga cgg ggt gag tta ctg atc tct ctc tgc	1038
120	Asn Val Arg Lys Ser Ser Gly Arg Gly Glu Leu Leu Ile Ser Leu Cys	
121	285 290 295	
123	tat cag tcc acc aca aac act cta act gtg gtt gtc tta aaa gct cga	1086
124	Tyr Gln Ser Thr Thr Asn Thr Leu Thr Val Val Leu Lys Ala Arg	
125	300 305 310	
127	cat ctg cct aaa tct gat gtg tcc gga ctt tca gat ccc tat gtc aaa	1134
128	His Leu Pro Lys Ser Asp Val Ser Gly Leu Ser Asp Pro Tyr Val Lys	
129	315 320 325	
131	gtg aac ctg tac cat gcc aaa aag aga atc tcc aag aag aag act cat	1182
132	Val Asn Leu Tyr His Ala Lys Lys Arg Ile Ser Lys Lys Lys Thr His	
133	330 335 340	
135	gtg aag aaa tgc acc ccc aat gca gtg ttc aat gag ctg ttt gtc ttt	1230

RAW SEQUENCE LISTING DATE: 10/18/2000
PATENT APPLICATION: US/09/680,121 TIME: 17:20:29

Input Set : A:\Mueth31.app
Output Set: N:\CRF3\10182000\I680121.raw

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/680,121

DATE: 10/18/2000
 TIME: 17:20:29

Input Set : A:\Mueth31.app
 Output Set: N:\CRF3\10182000\I680121.raw

```

223 ttaaaaatgga taatttgtaa atagttttaa gcttttaaaa tttaaagtgt ttttgagtgt 3455
225 gaaaaggtaa gtaaaaactat ttgcaactgg ttttcagaaa agagaaaaga aacaacaaag 3515
227 gaatttggaaac aggccaggag atcttaatac ctaatttcat catttctgca aatgtactg 3575
229 tttagaatg tattacaata tcaatgtgaa tacatgtgaaatcttgcataa atcctgcact 3635
231 gtatcaaaca tgtaaaattaa ttgttgtct gattagccaa ttcacacc caaatggga 3695
233 ggtatacatg ttgttgaagaaac gtgttaactcg gtaatgtt gttctgtatg ttgttaactca 3755
235 atagaagtgt ttgttgaagga agcatgtgt gtgagacagt gtctgttctt ttgtgccagc 3815
237 tctgtatgat ttgttgaaga ccatgtttgt-aagacatgaa taaattgtgt ctggccca 3875
239 aaaaaaaaaa aaaaaaa 3891
242 <210> SEQ ID NO: 2
243 <211> LENGTH: 425
244 <212> TYPE: PRT
245 <213> ORGANISM: Homo sapiens
246 <223> OTHER INFORMATION: product = Repro-PC-1.0
248 <400> SEQUENCE: 2
249 Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
250 1 5 10 15
252 Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
253 20 25 30
255 Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
256 35 40 45
258 Pro Pro Tyr Lys Phe Val His Val Leu Lys Gly Val Asp Ile Tyr Pro
259 50 55 60
261 Glu Asn Leu Asn Ser Lys Lys Phe Gly Ala Asp Asp Lys Asn Glu
262 65 70 75 80
264 Val Lys Asn Lys Pro Ala Val Pro Lys Asn Ser Leu His Leu Asp Leu
265 85 90 95
267 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
268 100 105 110
270 Gly Ser Pro Ser Asp Leu Glu Asn Ala Thr Pro Lys Leu Phe Leu Glu
271 115 120 125
273 Gly Glu Lys Glu Ser Val Ser Pro Glu Ser Leu Lys Ser Ser Thr Ser
274 130 135 140
276 Leu Thr Ser Glu Glu Lys Gln Glu Lys Leu Gly Thr Leu Phe Phe Ser
277 145 150 155 160
279 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
280 165 170 175
282 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
283 180 185 190
285 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
286 195 200 205
288 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
289 210 215 220
291 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
292 225 230 235 240
294 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
295 245 250 255
297 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
298 260 265 270

```

09/680, 121

P.6

<210> 11 Seg # 11

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> residue 1=Thr, Ser or Met

<220>

<223> residue 2=Asp, Glu, Ala, Ser or Thr

<400> 11

(Xaa) (Xaa) Xaa Xaa Xaa Xaa Xaa Xaa Tyr

1 5

OK



All "Xaa's" in the sequence
must be explained. See #10
on Error Summary Sheet.

This error is indicated throughout
the sequence listing.

↙ F.4.1.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 10/18/2000
PATENT APPLICATION: US/09/680,121 TIME: 17:20:30

Input Set : A:\Mueth31.app
Output Set: N:\CRF3\10182000\I680121.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:648 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:648 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:648 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:664 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:664 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:664 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:677 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:677 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:677 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:690 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:690 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:690 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:707 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:707 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:707 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:724 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:16
L:724 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:16
L:724 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:737 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:737 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:737 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:750 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:18
L:750 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:18
L:750 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:766 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:766 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:766 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:779 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:779 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:779 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:885 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:27
L:885 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:885 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:27



Creation date: 12-20-2003

Indexing Officer: TBUI1 - THU-TRANG BUI

Team: OIPEBackFileIndexing

Dossier: 09680121

Legal Date: 11-11-2002

No.	Doccode	Number of pages
1	C.AD	1

Total number of pages: 1

Remarks:

Order of re-scan issued on